

FIG.1

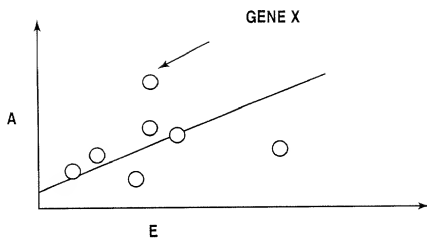


FIG.2

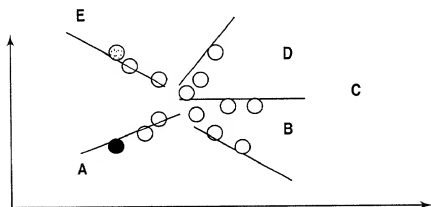


FIG.3

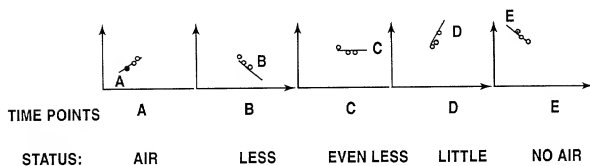



FIG.4

Please, log in

**array SCOUT™**

Login

lion

Password

\*\*\*\*

Account

lion

OK Cancel

00754120 000001

**Ready**

Fig.6

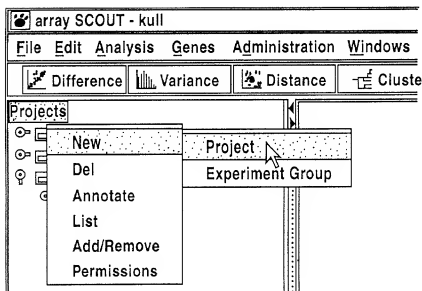


Fig.7

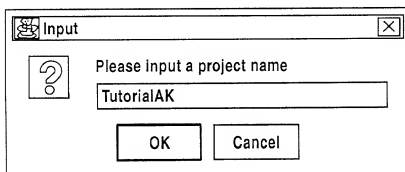


Fig.8

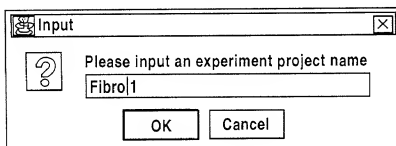


Fig.9

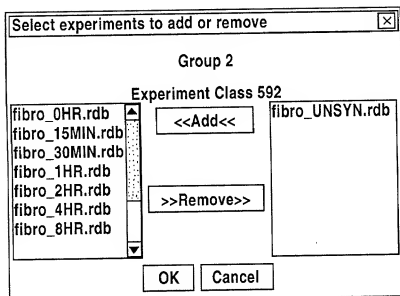


Fig.10

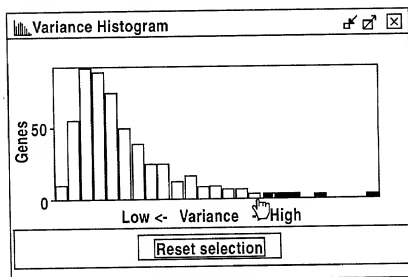


Fig.11

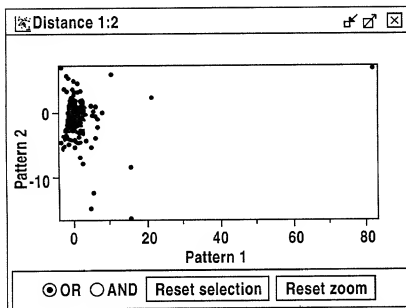


Fig.12

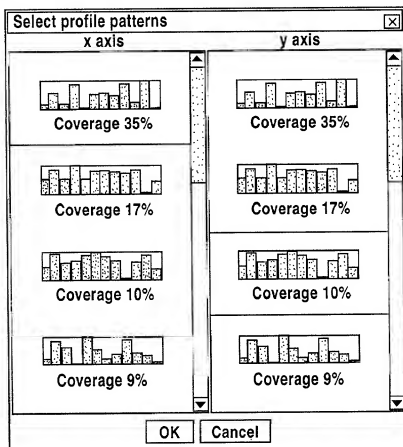


Fig.13

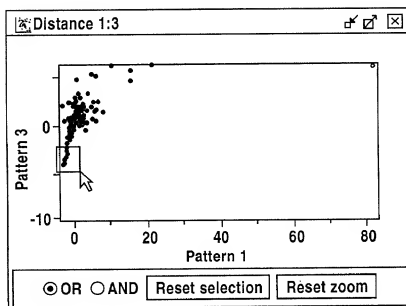


Fig.15

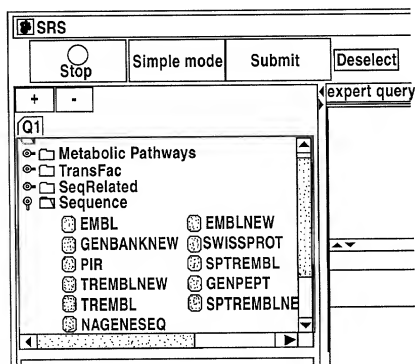


Fig.14

Gene	Description	Selected in
W72759	zd71h04.s1 Soares fetal heart NbHH19W Homo sapie...	◆
R40626	yf72g12.s1 Homo sapiens cDNA clone 28051 3'.	◆
AA001916	zh83b05.s1 Soares fetal liver spleen 1NFLS 5'1 Homo...	◆
R43728	yg20c12.s1 Homo sapiens cDNA clone 32811 3'.	◆
AA041370	zf09a02.s1 Soares fetal heart NbHH19W Homo sapie...	◆
T95837	ye42c02.s1 Homo sapiens cDNA clone 120386 3'.	◆
H27557	yl61g03.s1 Homo sapiens cDNA clone 162772 3' simi...	◆
AA024572	ze76h08.s1 Soares fetal heart NbHH1 9W Homo sapie...	◆



Fig.16

☐ Stop
 ☐ Simple mode

Q1

ys

EW

W

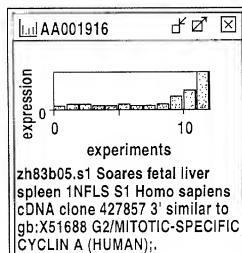
Q

☐ EMBLNEW
 ☐ SWISSPROT
 ☐ SPTREMBL
 ☐ GENPEPT
 ☐ SPTREMBLNEW

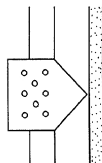
☐ GENBANK
 ☐ SWISSNEW
 ☐ REMTREMBL
 ☐ GENPEPTNEW
 ☐ AAGENESEQ

Description ▼ cyclin

Fig.17



**Fig.18**



**Scale Tab**

**Fig.19**



**Cluster 1**

**Cluster G**

**Cluster E**

**Cluster C**

**Cluster B**

**Cluster A**

Fig.20

### Projects

-   Bertrand
-   fibroblast data
-   Fibroblast Project
-   Illico Presto

Fig.21










-   Experiment group 1
  -  experiment 0 min
  -  experiment 15 min
  -  experiment 30 min
  -  experiment 1h
  -  experiment 2h

Fig.22

 Input ✕

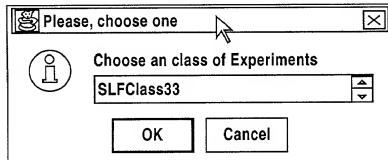


Please input an experiment group name

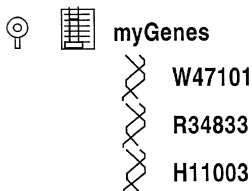
Experiment group name dialog box.

**Fig.23**

Choose experiment class dialog box.

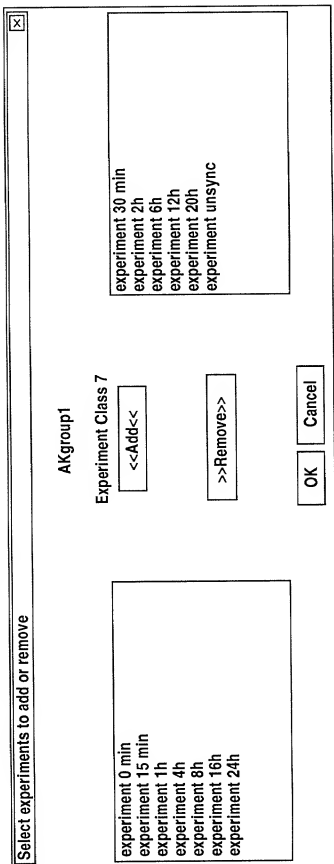


**Fig.25**



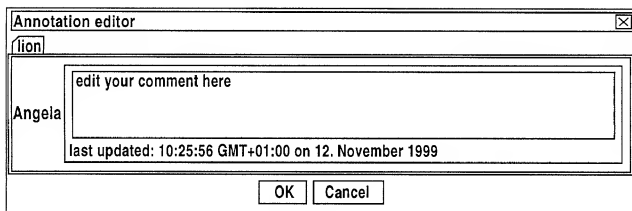
**Fig. 24**

**Add/Remove dialog box for adding and removing experiments from experiment groups.**



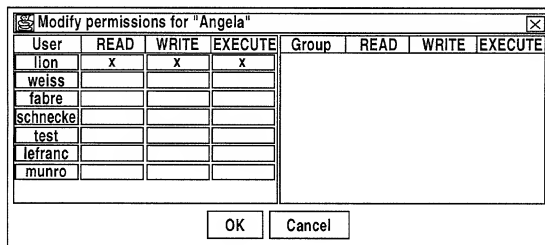
# Fig.26

The annotation editor.



# Fig.27

The permissions dialog box for project "Angela".



# Fig.28

Select parameters "Data Scaling" dialog box.

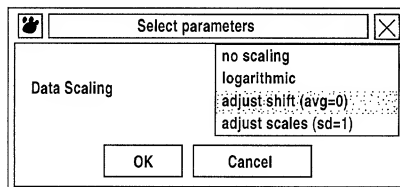


Fig.29

The Choose experiments dialog box.

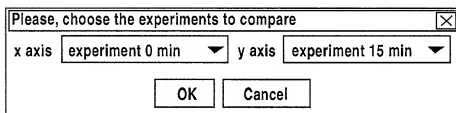


Fig.30

An example difference plot.

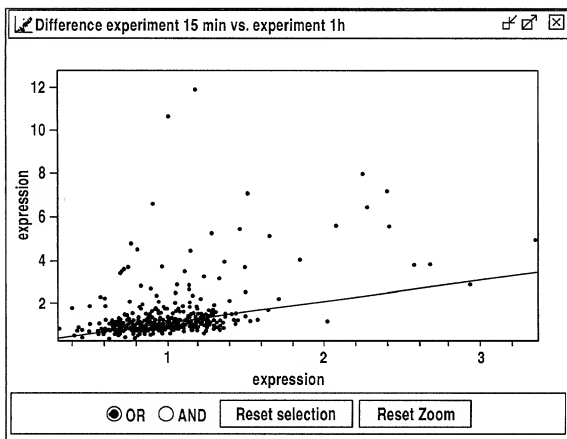


Fig.31

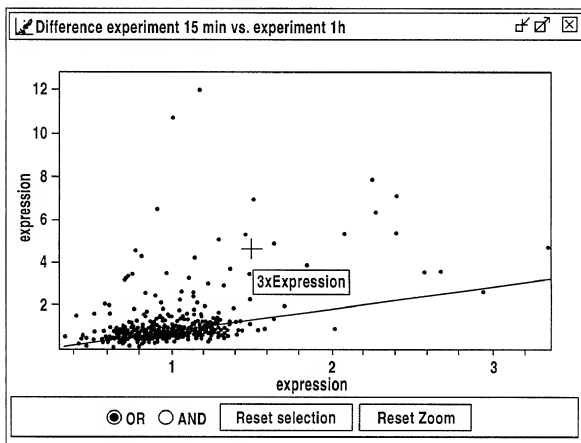




Fig.32

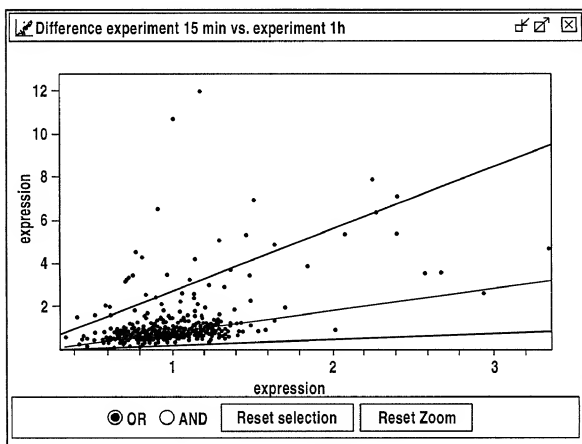
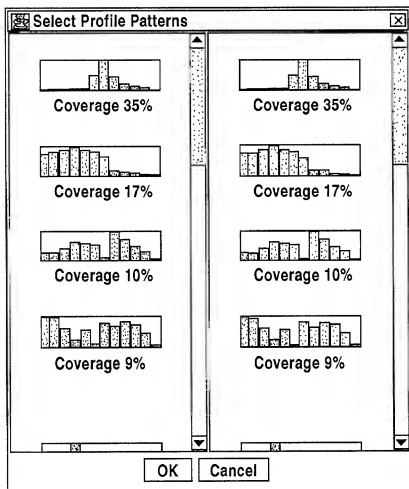


Fig.33

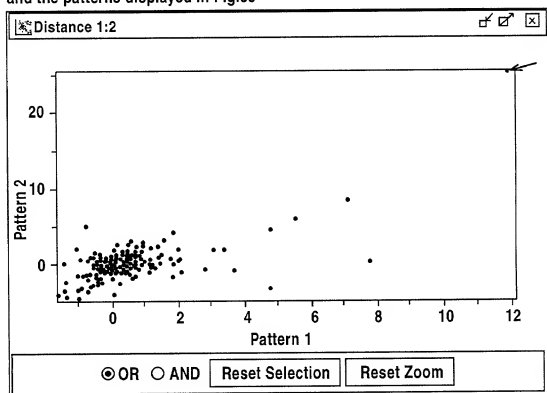
Select Profile Patterns dialog box.



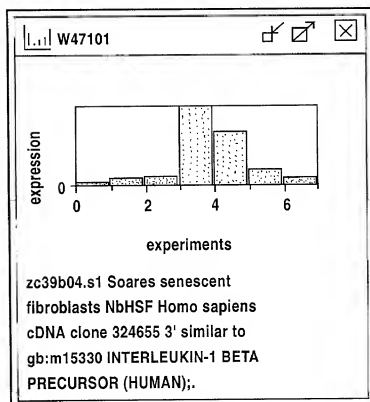
# Fig.34

Gene profiled in Fig.35

Distance Plot created with the adjust shift (avg=0) scaling procedure and the patterns displayed in Fig.33



# Fig.35



Gene Profile of gene W47101 plotted at (12,26) in the above Distance Plot (Figure 34).

**Fig.36**

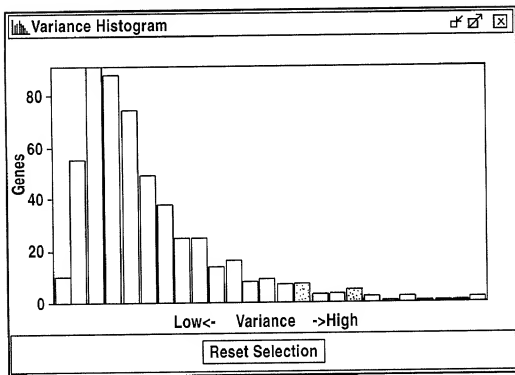
The "Select Experiments to plot" dialog box for the variance histogram.

Experiment	Include	Exclude
experiment I	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment II	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment III	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment IV	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment V	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment VI	<input checked="" type="checkbox"/>	<input type="checkbox"/>
experiment VII	<input checked="" type="checkbox"/>	<input type="checkbox"/>

OK Cancel

# Fig.37

The Variance Histogram with two bars selected.



# Fig.38

The "Enter Correlation Values" dialog box.

Experiment	Target Value
experiment 0 min	1
experiment 15 min	1
experiment 30 min	1
experiment 1h	1
experiment 2h	1
experiment 3h	1
experiment 6h	1
experiment 8h	1
experiment 12h	10.0
experiment 16h	1
experiment 20h	1
experiment 24h	1

OK Cancel

Fig.39

Correlation histogram parameters dialog box.

Correlation histogram parameters dialog box.

Select parameters

Target Scaling

- no scaling
- logarithmic range
- unit range

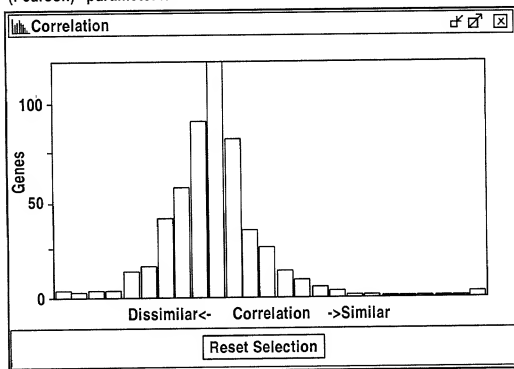
Comparison Method

- by Shape (Pearson)
- by absolute values

OK Cancel

Fig.40

A correlation histogram created using the "no scaling" and the "by Shape (Pearson)" parameters.



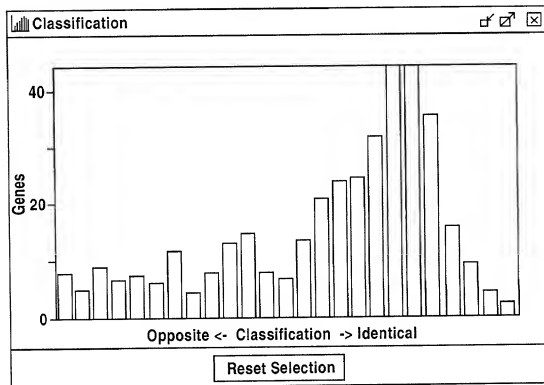
# Fig.41

The "Classify Experiments" dialog box.

Experiment	Positive	Negative	Exclude
WT, liquid (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
WT (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
WT, solid (ave)	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
KO (ave)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

OK Cancel

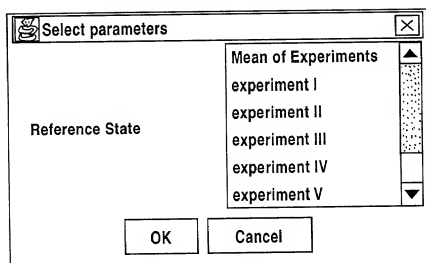
# Fig.42



The Classification histogram created using the "adjust scales" scaling procedure and the data displayed in the "Classify Experiments" dialog box above (Figure 41).

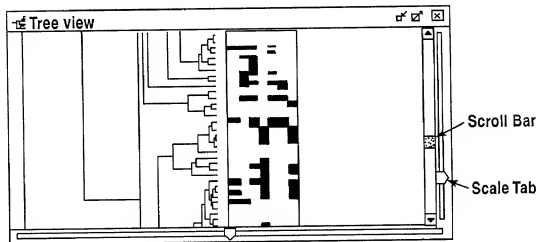
# Fig.43

Select reference state dialog box.



# Fig.44

The Cluster Tree analysis view.





# Fig.45

The SRS Interface In Simple Mode.

☐ Stop

Detail mode

Query on pathway

Query on swissprot alone

retrieve possible human sequences  
 retrieve sequences with nucleotide b  
 search mutation database

Num	Db	ID	Description
1	SWISSPROT	AC01_YEAST	
2	SWISSPROT	ACR1_YEAST	
3	SWISSPROT	ACR3_YEAST	
4	SWISSPROT	ADB1_YEAST	
5	SWISSPROT	ADB1_YEAST	

keyword:

19950912 12:52:50

SRS

Stop

Simple mode

Submit

Deselect

+

-

Q1

☐ all dbs  
☒ Metabolic Pathways  
☒ TransFac  
☒ SeqRelated  
☒ Sequence  
☐ EMBL  
☐ EMBLNEW  
☐ GENBANKNEW  
☐ PIR  
☐ TREMBLNEW  
☐ TREMBL  
☐ SPTREMBL  
☐ GENPEPT  
☐ SPTREMBLNEW

Query on swissprot alone

Num	Db	ID
1	SWISSPROT	AP17_YEAST
2	SWISSPROT	FT11_YEAST
3	SWISSPROT	IM17_YEAST
4	SWISSPROT	IM22_YEAST
5	SWISSPROT	IM23_YEAST
6	SWISSPROT	IM44_YEAST
7	SWISSPROT	IM17_YEAST

[http://bssever1/srs6bin/cgi-bin/wgetz?+=\[SWISSPROT-ID:IM17\\_YEAST\]](http://bssever1/srs6bin/cgi-bin/wgetz?+=[SWISSPROT-ID:IM17_YEAST])

Back

Forward

SWISSPROT:IM17\_YEAST

ID

IM17\_YEAST

AC

P39515; Q02310;

DT

01-FEB-1995 (Rel. 31, Created)

DT

01-FEB-1995 (Rel. 31, Last sequence update)

DT

15-JUL-1998 (Rel. 36, Last annotation update)

DE

MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE S

DE

(MITOCHONDRIAL PROTEIN IMPORT PROTEIN 2) (MITOCHO

DE

PROTEIN MIM17).

GM

TIM17 OR IM17 OR MIM17 OR SMI1 OR YJL143W OR JO64

STANDARD:

PRT: 158 AA.

Description

membrane

+

The software SRS interface in Detail Mode displaying a completed query and a database entry.

Fig.46

Fig.47

RDB and text Files (\*.rdb and \*.txt)

No file selected...

Existing class Define a new class experiment

New class name

Type of class

No identifiers File selected

Add an identifiers file

Experiment name

Select a File... Import... Cancel

Fig.48

RDB and text Files (\*.rdb and \*.txt)

No file selected...

Existing class Define a new class experiment

List of the existing experiment classes

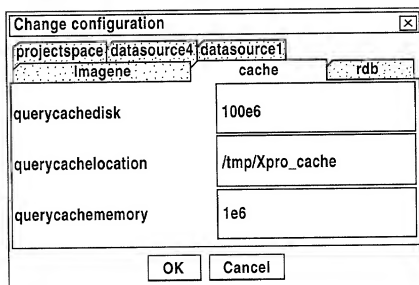
dkfz data, average  
dkfz data  
tabTestData  
Ustilago MTP  
Ustilago

Experiment name

Select a File... Import... Cancel

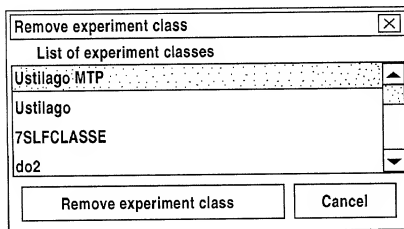
# Fig.49

Change configuration dialog box.



# Fig.50

Remove experiment class dialog box.



# Fig.51

Remove experiments dialog box.

Remove experiments

List of experiment classes

Ustilago MTP

Ustilago

List of all experiments for the selected class

MTP-OD0\_5-c

MTP-WT-a

MTP-WT-b

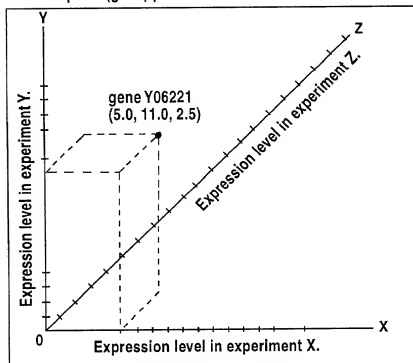
MTP-WT-ave

Remove experiments

Cancel

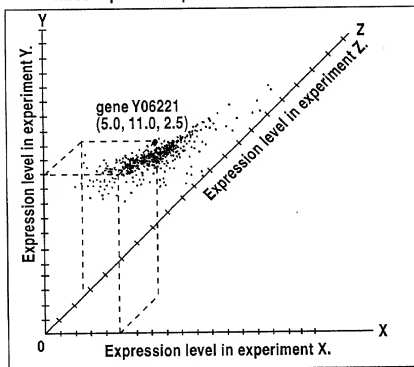
# Fig.52

A point (gene) plotted in three dimensions.



**Fig.53**

Three experiments plotted in 3 dimensions.



**Fig.54**

Squash the cigar along its side to best preserve its shape.

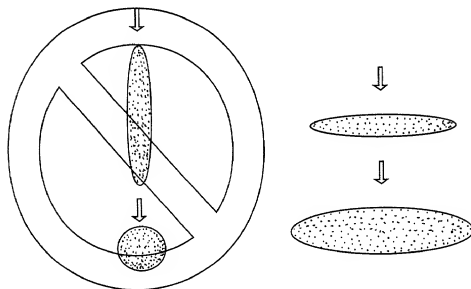


FIG.55

GENERAL FLOW CHART ARRAY ANALYSIS

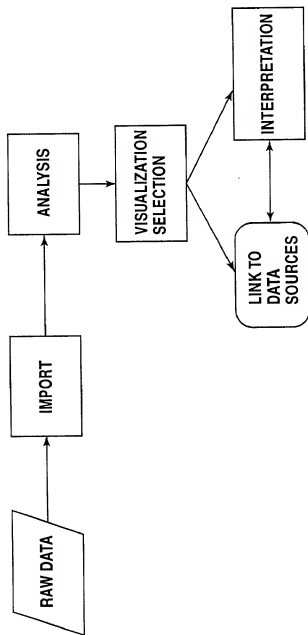


FIG.56

ANALYSIS OF SEVERAL UNCHARACTERIZED SAMPLES

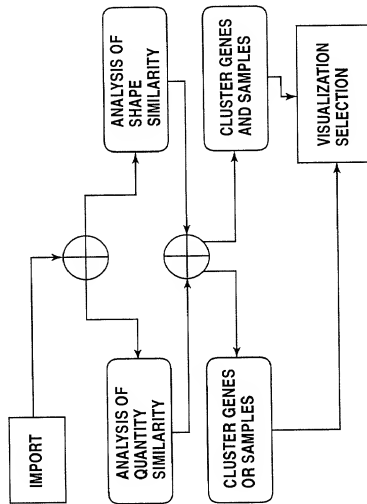




FIG.57

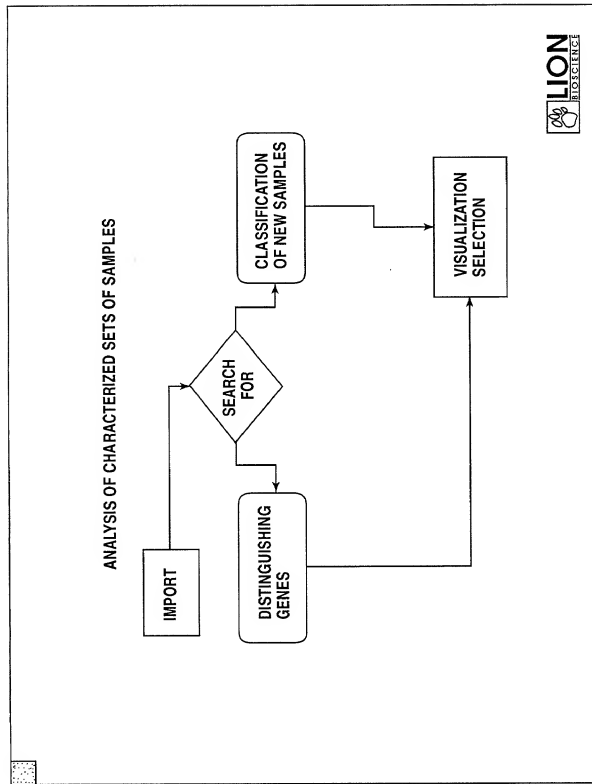


FIG.58

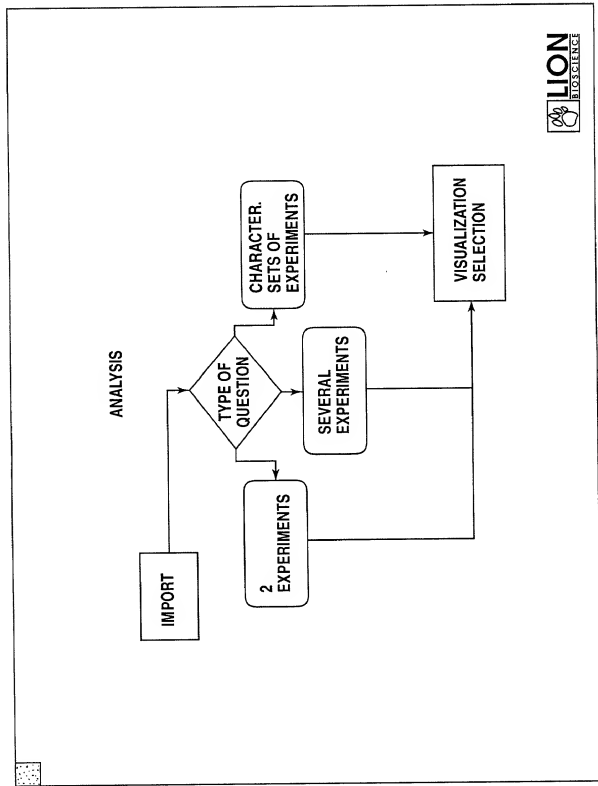


FIG.59

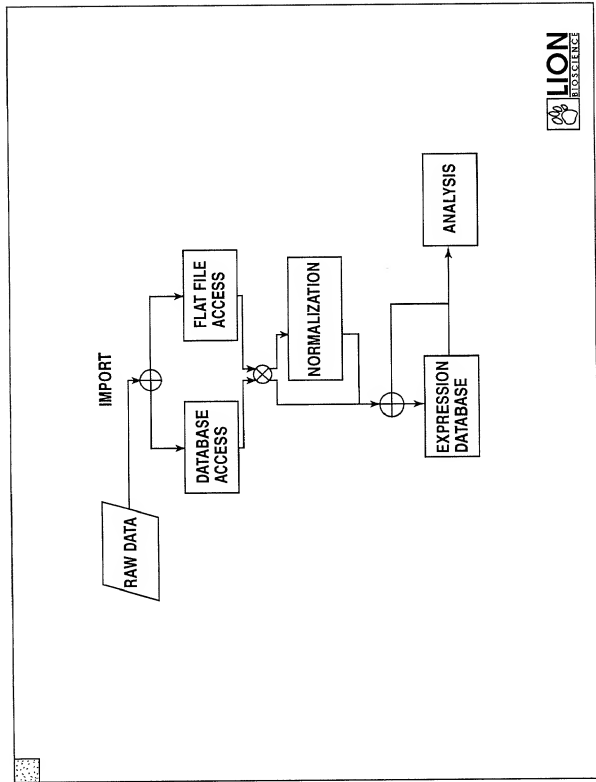
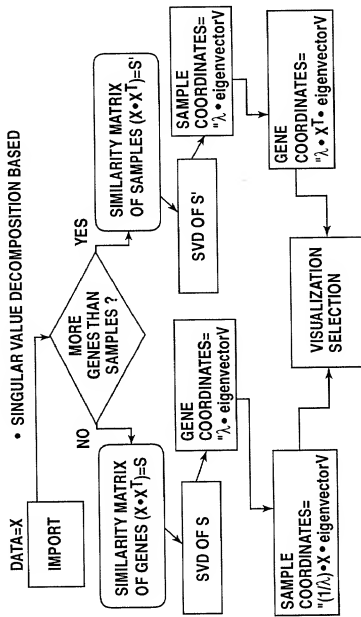


FIG.60

## SIMULTANEOUS ANALYSIS OF GENE AND SAMPLE SIMILARITY

• SINGULAR VALUE DECOMPOSITION BASED



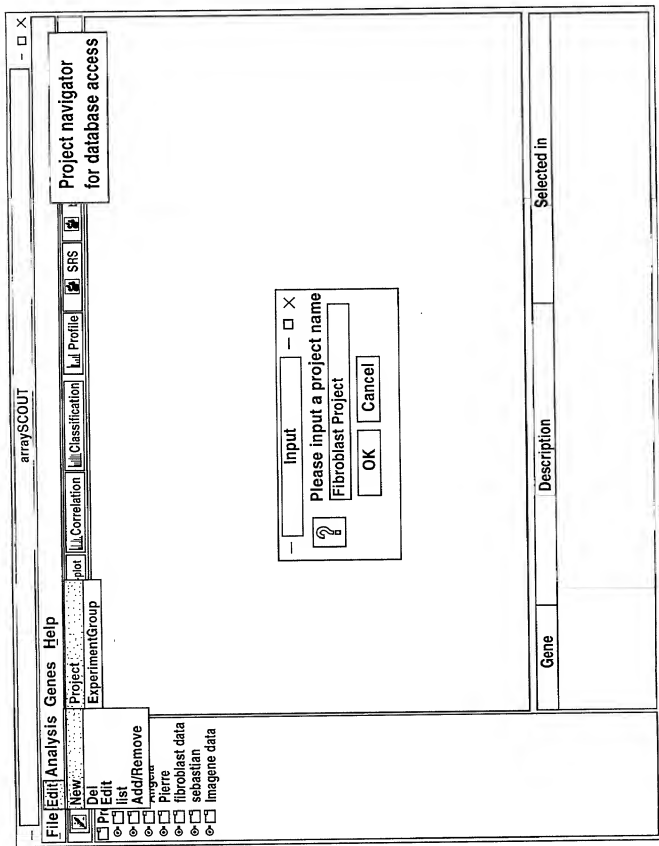
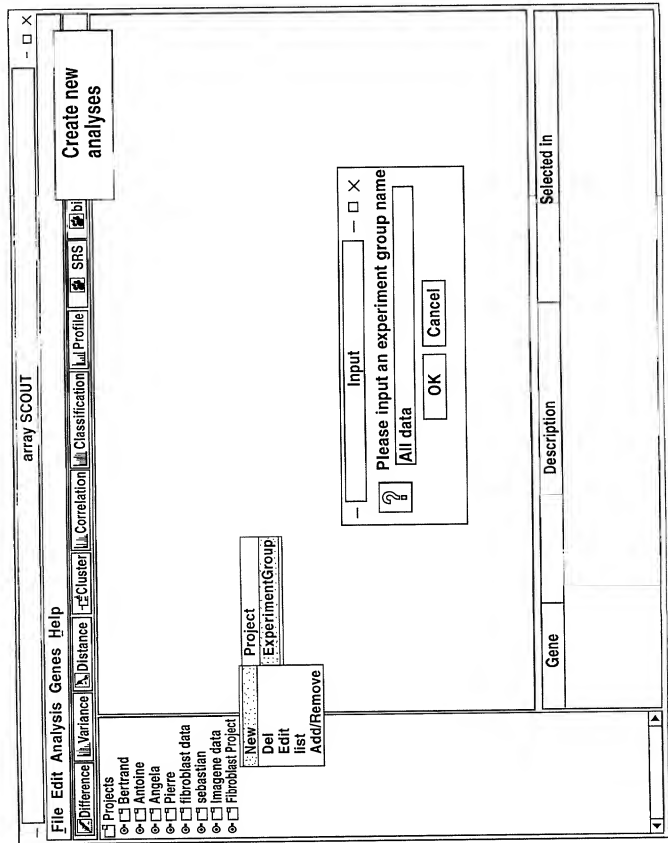


FIG.61

FIG.62



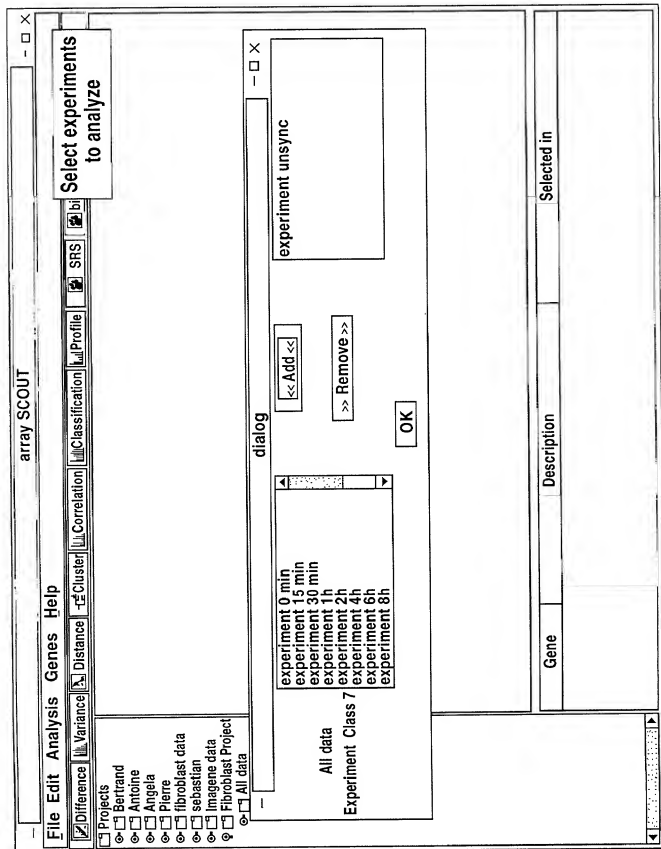


FIG.63

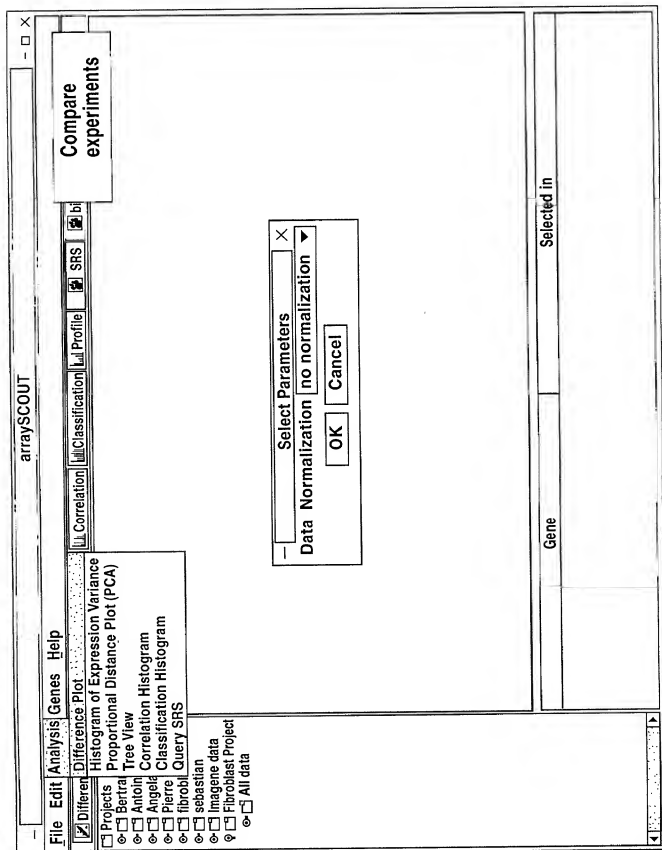


FIG.64



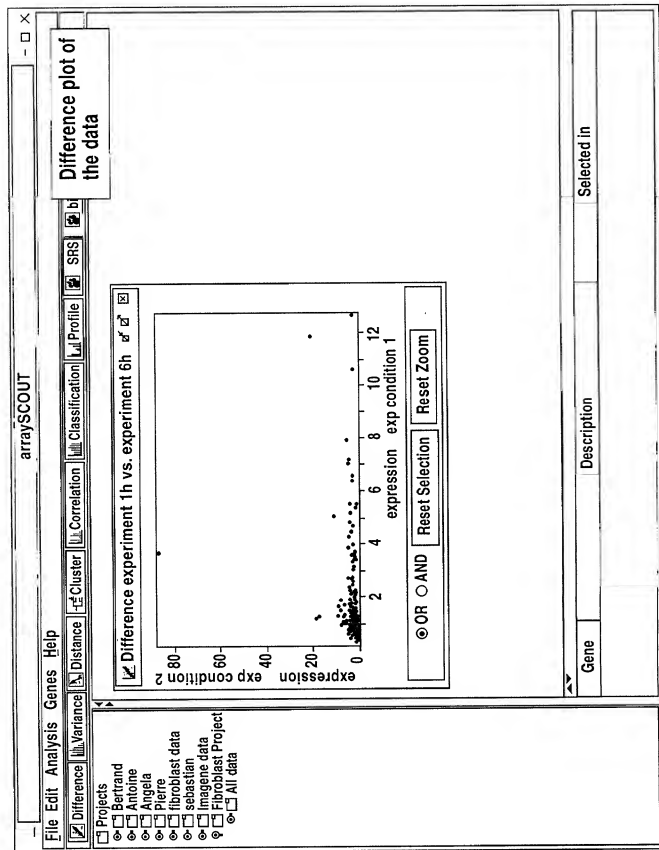
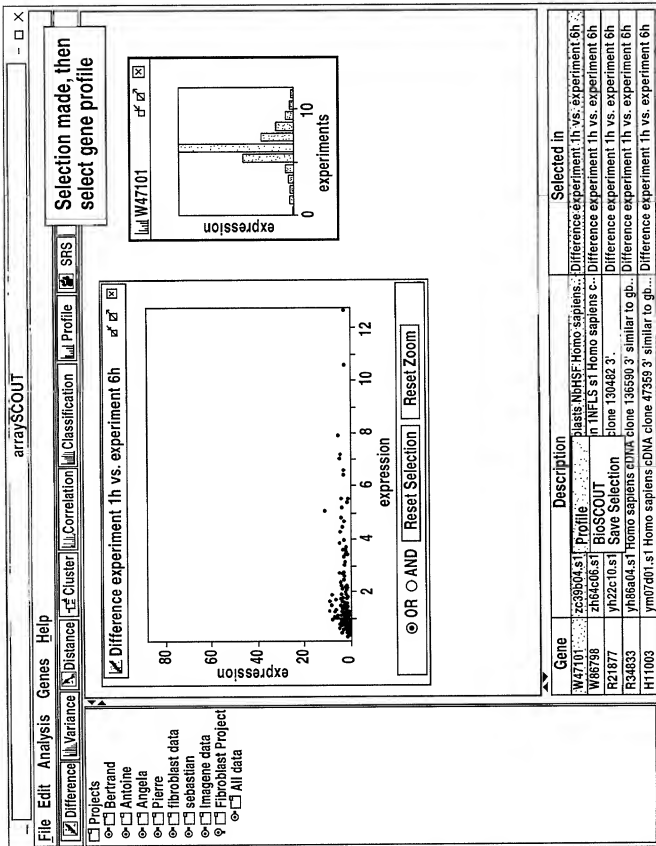


FIG.65

FIG.66



**arraySCOUT**

File Edit Analysis Genes Help

☒ Difference 
 ☒ Variance 
 ☒ Distance 
 ☒ Cluster 
 ☒ Correlation 
 ☒ Classification 
 ☒ Profile

☒ Projects  
☒ Bertrand  
☒ Antoine  
☒ Angela  
☒ Pierre  
☒ fibroblast data  
☒ sebastian  
☒ imagine data  
☒ Fibroblast Project  
☐ All data

Display and select within other views on the data

ludl T95837

Difference experiment 1h vs. experiment 6h

expression

expression

OR AND Reset Selection

Reset Zoom

Selected In

Gene	Description
T95837	yel2c20.s1 Homo sapiens cDNA clone 120385 3'
H27557	y167g30.s1 Homo sapiens cDNA clone 162772 3' similar to ...
W47101	zc39b04.s1 Soares senescent fibroblasts N2F7R2 Homo sapiens...
W68798	zh64c06.s1 Soares fetal liver spleen INFLS S1 Homo sapiens c...
R21877	yh22c10.s1 Homo sapiens cDNA clone 130482 3'
R34633	yh86a04.s1 Homo sapiens cDNA clone 136590 3' similar to gb...
H11003	ym7d01.s1 Homo sapiens cDNA clone 47359 3' similar to ...
AA016304	zc38c08.s1 Soares retina N25-4HR Homo sapiens cDNA clone...
W88807	zh71b12.s1 Soares fetal liver spleen INFLS S1 Homo sapien...
W90037	zh69H11.s1 Soares fetal liver spleen INFLS S1 Homo sapien...

Difference experiment 1h vs. experiment 12h  
 Difference experiment 1h vs. experiment 12h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 6h  
 Difference experiment 1h vs. experiment 12h  
 Difference experiment 1h vs. experiment 12h  
 Difference experiment 1h vs. experiment 12h

**FIG. 67**

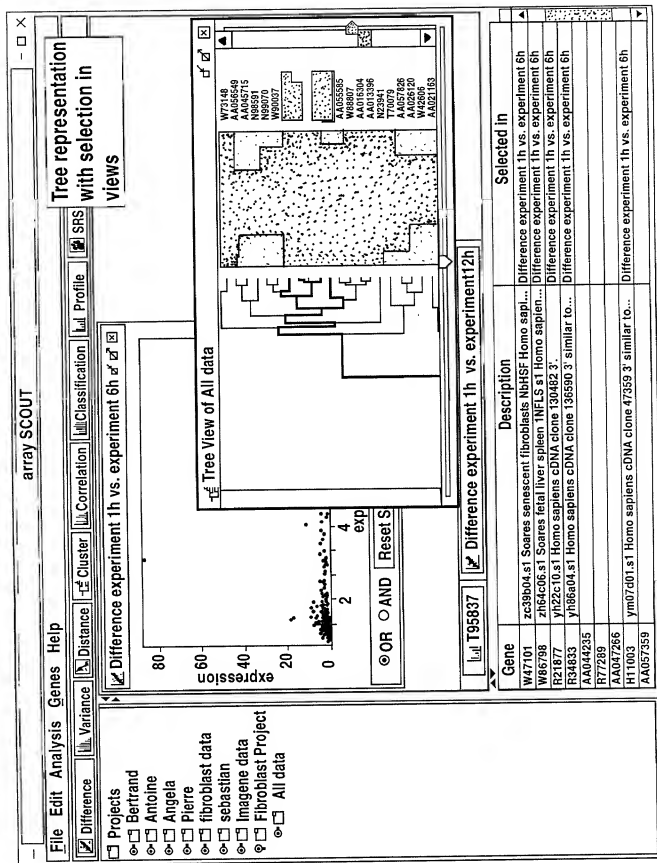


FIG.68

**array SCOUT**

---

**File Edit Analysis Genes Help**

☒ Difference    ☐ Variance    ☐ Distance    ☐ t-Cluster    ☐ Correlation    ☐ Classification    ☐ Profile    ☐ SRS    ☐ Compare profiles

---

☐ Projects  
☒ Bertrand  
☒ Antoine  
☒ Angela  
☒ Pierre  
☒ fibroblast data  
☒ sebastian  
☒ imagine data  
☒ Fibroblast Project  
☐ All data

---

**Difference experiment**

**W47101**

**H11003**

**R21877**

**W86798**

---

**OR AND Basic Selection Basic Zoom**

---

Gene	Description	Selected in
W47101	zc39b04.s1 Soares senescent fibroblasts NbHSF Homo sapi...	Difference experiment 1h vs. experiment 6h
W86798	zh64c06.s1 Soares fetal liver spleen 1NfLS s1 Homo sapie...	Difference experiment 1h vs. experiment 6h
R21877	y922c10.s1 Homo sapiens cDNA clone 130482.3'	Difference experiment 1h vs. experiment 6h
R34633	yH66a04.s1 Homo sapiens cDNA clone 136590.3' similar to...	Difference experiment 1h vs. experiment 6h
H11003	ym07d01.s1 Homo sapiens cDNA clone 47359.3' similar to...	Difference experiment 1h vs. experiment 6h

**FIG. 69**

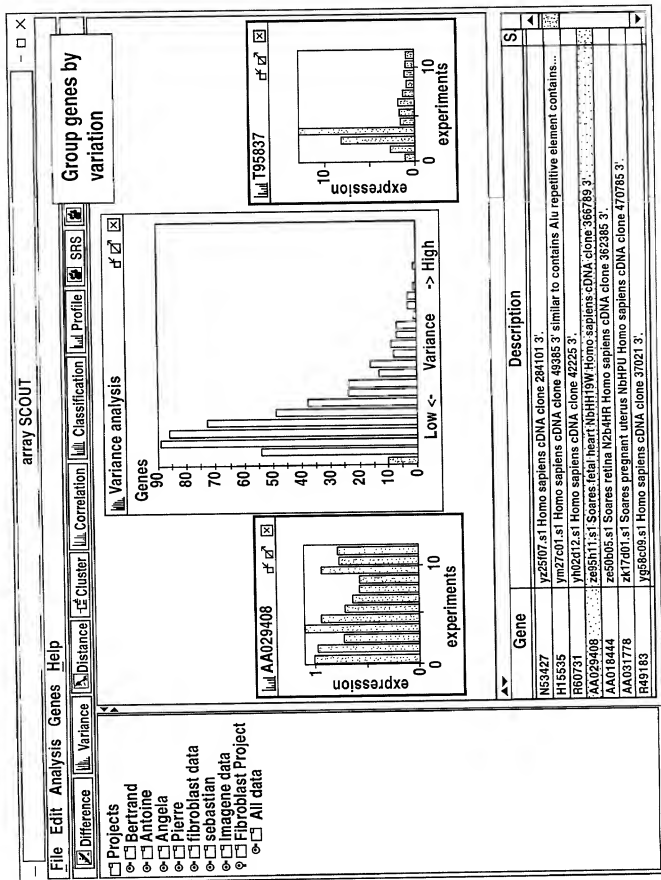


FIG.70

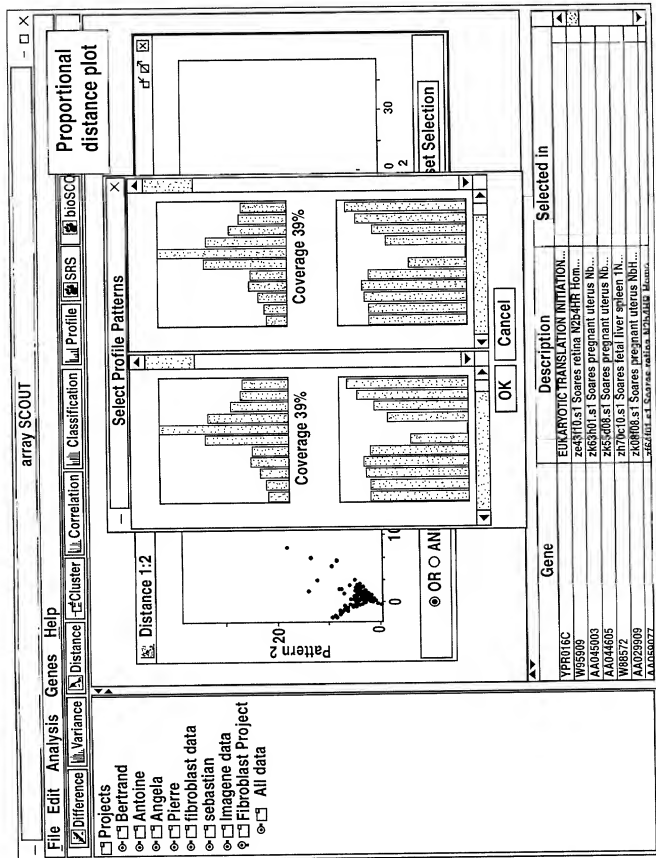


FIG.71

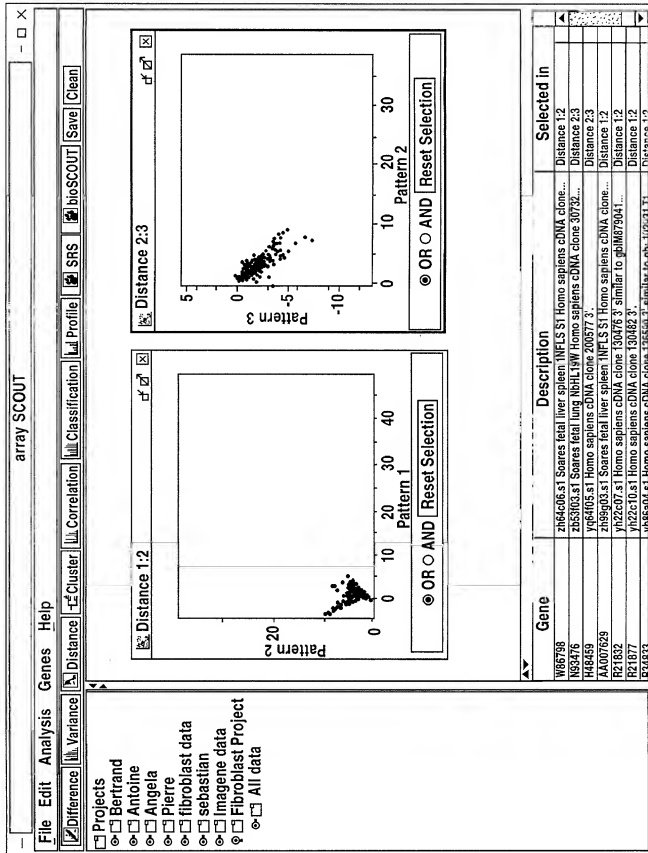


FIG.72



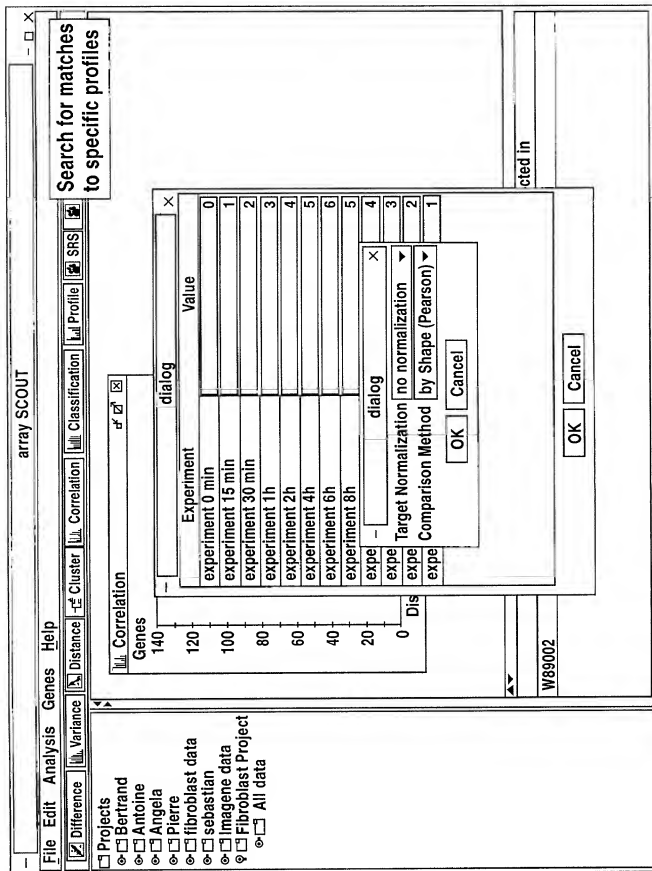


FIG.73

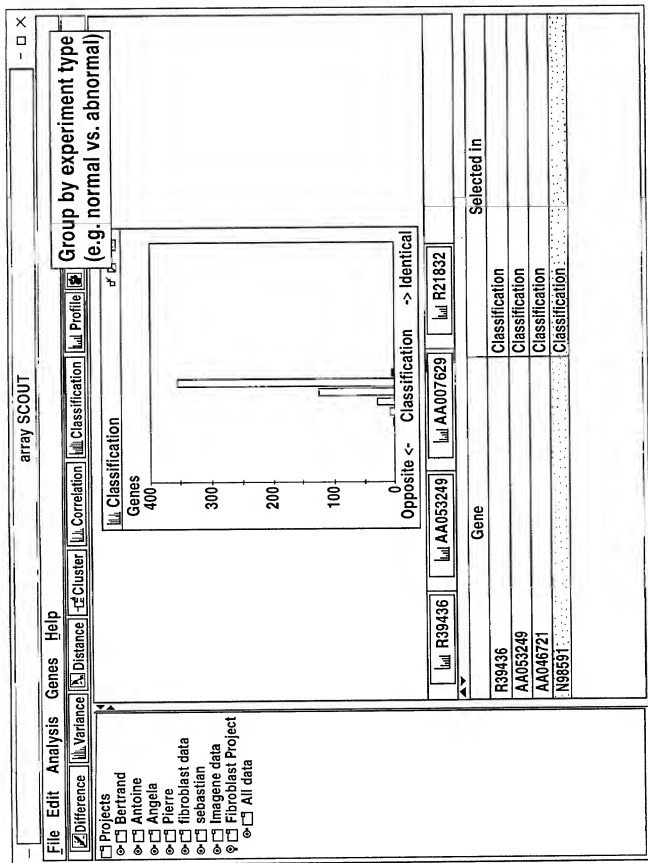
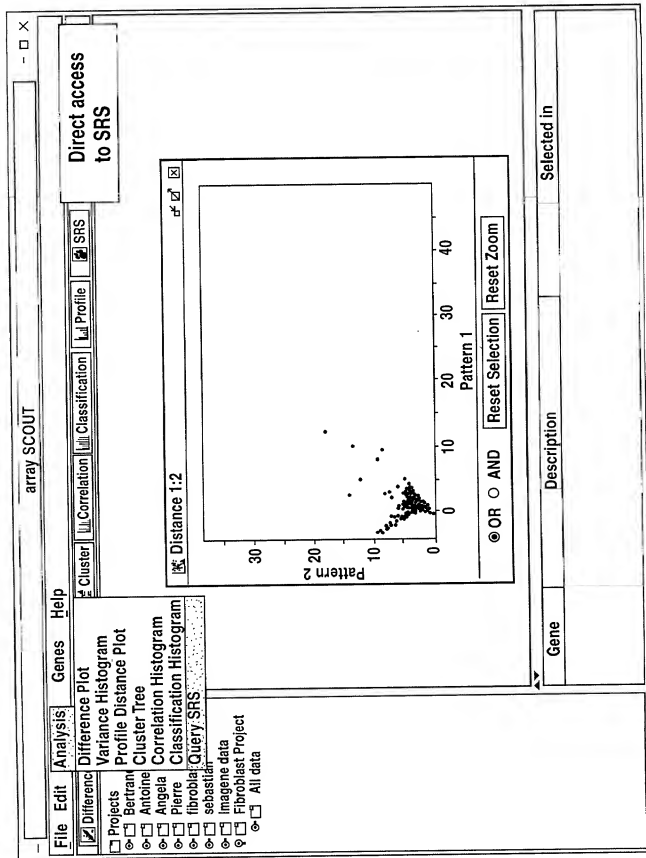


FIG.74



FIG.76



array SCOUT

File Edit Analysis Genes Help

☒ Difference ☐ Variance ☐ Distance ☒ Cluster ☐ Correlation ☐ Classification ☐ Profile ☒ SRS

SRS queries can be easily constructed using this interface

☒ SRS

☐ Stop  
☐ Simple mode  
☐ Submit  
☐ Deselect

Q1

☐ all dbs  
☐ SeqRelated  
☐ Protein3DStruct  
☐ Sequence  
☐ Mutations  
☐ TransFac  
☐ Mapping  
☐ Metabolic Pathways  
☐ Others

Back Forward

Projects

☐ Bertrand  
☐ Antoine  
☐ Angela  
☐ Pierre  
☐ fibroblast data  
☐ sebastian  
☐ Imagene data  
☒ Fibroblast Project  
☐ All data

Gene

☐ W85796  
☐ R21877  
☐ R34833  
☐ H11003

Description

zh64406.s1 Soares fetal liver spleen 1NFLS...  
 yf22510.s1 Homo sapiens cDNA clone 130...  
 yf86904.s1 Homo sapiens cDNA clone 136...  
 ym07401.s1 Homo sapiens cDNA clone 47...

Selected in

Distance 1:2  
 Distance 1:2  
 Distance 1:2  
 Distance 1:2

FIG.77

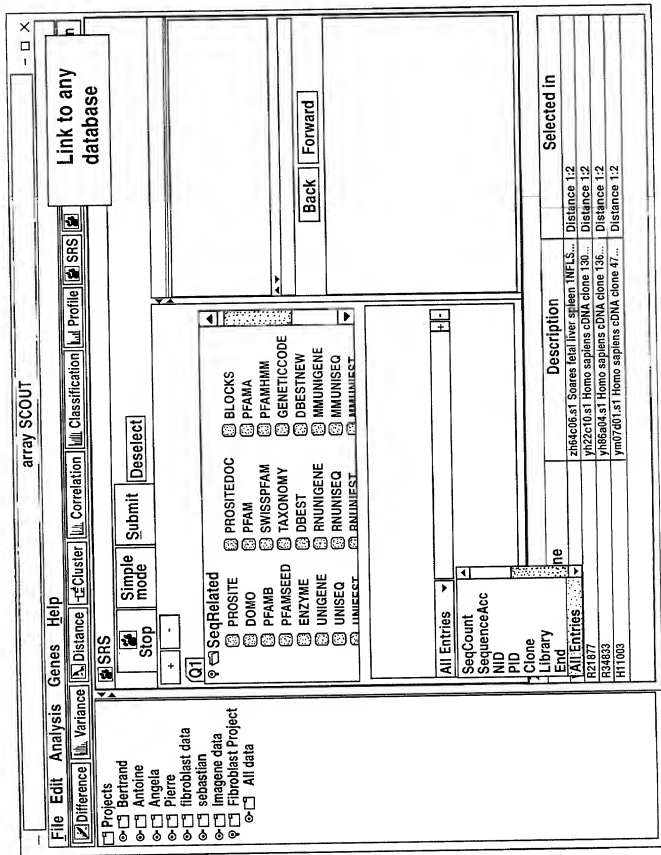


FIG.78

FIG.79

array SCOUT
- □ X

File
Edit
Analysis
Genes
Help

☒ Difference
 ☒ Variance

☒ Distance
 ☒ Cluster
 ☒ Correlation
 ☒ Classification
 ☒ Profile
 ☒ SRS

☐ Projects  
☐ Bertrand  
☐ Antoine  
☐ Angela  
☐ Pierre  
☐ fibroblast data  
☐ sebastian  
☐ Imagene data  
☐ Fibroblast Project  
☐ All data

☒ SeqRelated  
☒ Protein3DStruct  
☒ Sequence  
☒ EMBL  
☒ GENBANKNEW  
☒ PIR  
☒ TREMBLNEW  
☒ TREMBL  
☒ NACENESEQ  
☒ EMBLNEW  
☒ SWISSPROT  
☒ SPTREMBL  
☒ GENPEPT  
☒ GENPEPTNEW  
☒ SPTREMBL  
☒ AAGENESEQ  
☒ NEW

☒ Simple mode  
☐ Stop  
☐ Submit  
☐ Deselect

☐ Q1-> Q2  
☐ Q1-> Q3  
☐ Q1-> Q4

array SCOUT

File Edit Analysis Genes Help

☒ Difference ☒ Variance ☒ Distance ☒ Cluster ☒ Correlation ☒ Classification ☒ Profile ☒ SFS

**Results displayed**

☒ Projects  
☐ Bertrand  
☐ Antoine  
☐ Angela  
☐ Pierre  
☐ fibroblast data  
☐ sebastian  
☐ Imagine data  
☐ Fibroblast Project  
☐ All data

**SFS**

☒ Stop ☐ Simple mode ☐ Submit ☐ Deselect

☒ Q1 > Q2  
☐ SeqRelated  
☐ Protein3DStruct  
☐ Sequence  
☐ EMBL  
☐ GENBANKNEW  
☐ PIR  
☐ TREMBLNEW  
☐ TREMBL  
☐ SWISS  
☐ SPTR

Num Db ID Description  
 1 SWISSPROT SY02 HUMAN

[http://bserver1/srs6bin/cqt-bin/wgetz?-e+{SWISSPROT-ID:SY02\\_HUMAN}](http://bserver1/srs6bin/cqt-bin/wgetz?-e+{SWISSPROT-ID:SY02_HUMAN})

Back Forward

function subgit(form,addE) {form.elements.form.elements.  
 View length-1};

\* Complete entries\*

SWISSPROT:SY02\_HUMAN

ID SY02 HUMAN STANDARD; PRT; 99 AA.  
 AC P13500;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

Gene	Description	Distance
T77877	YD20H11.3 Homo sapiens cDNA clone 677	Distance 1:2
W85796	ZNF406.31 Sorens fetal liver spleen INFLS	Distance 1:2
R21877	YD22T10.31 Homo sapiens cDNA clone 130	Distance 1:2
R34833	YH8604.31 Homo sapiens cDNA clone 136	Distance 1:2
H11003	YH07401.31 Homo sapiens cDNA clone 47...	Distance 1:2

AllText - cytokine

FIG.80







[illegible]